

10/591464

SEQUENCE LISTING

<110> Method for screening of filamentous fungus-specific antimicrobial agents and kit for the screening

<120> RIKEN

<130> PH-2421-PCT

<150> JP 2004-061273

<151> 2004-03-04

<160> 17

<170> PatentIn Ver. 2.1

<210> 1

<211> 5457

<212> DNA

<213> Magnaporthe grisea

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<212> DNA

<213> Artificial Sequence

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<210> 4

<211> 37

<212> DNA

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<223> Description of Artificial Sequence:

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<210> 5
<211> 35
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<211> 31
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<210> 8

<211> 37

<212> DNA

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<223> Description of Artificial Sequence:

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<210> 12
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<212> DNA

<213> Artificial Sequence

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tttctcgagt tataggtttg tggtgtaata ttttagat 37

<210> 14

<211> 35

<212> DNA

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<213> Magnaporthe grisea

<400> 16

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20 25 30

Ser Thr Tyr Val Gln Leu Pro Gly Pro Glu Ser Asp Glu Lys Lys Gln
35 40 45

Leu Glu Arg Glu Leu Ala Ala Leu Val Ile Arg Val Gln Gln Leu Glu
50 55 60

Thr Arg Ala Asn Ala Ala Pro Ala Thr Ile Phe Pro Asp Thr Pro Asn
65 70 75 80

Glu Thr Ala His Ser Leu Phe Gly Asp Asp Ser Ser Ser Pro Thr Ser
85 90 95

Ser Ser Ser Gly Arg Glu Pro Lys Arg Leu Lys Ser Ala Ser Ser Thr
100 105 110

Thr Arg Asn Gly Phe Thr Thr Asp Gly Arg Pro Ser Lys Leu Asn Ala
115 120 125

Ile Thr Asp Glu Glu Leu Glu Gly Leu Arg Glu His Val Asp Gly Gln
130 135 140

Ser Arg Leu Leu Asp Ser Gln Arg Ala Glu Leu Asp Gly Val Asn Ala
145 150 155 160

Gln Leu Leu Glu Gln Lys Gln Leu Gln Glu Arg Ala Leu Ala Ile Ile
165 170 175

Glu Gln Glu Arg Val Ala Thr Leu Glu Arg Glu Leu Trp Lys His Gln
180 185 190

Lys Ala Asn Glu Ala Phe Gln Lys Ala Leu Arg Glu Ile Gly Ser Ile
195 200 205

Val Thr Ala Ala Ala Arg Gly Asp Leu Ser Lys Arg Val Lys Ile Asn
210 215 220

Pro Ile Glu Met Asp Pro Glu Ile Thr Thr Phe Lys Arg Thr Met Asn
225 230 235 240

Ala Met Met Asp Gln Leu Gly Val Phe Ser Ser Glu Val Ser Arg Val
245 250 255

Ala Arg Glu Val Gly Thr Glu Gly Ile Leu Gly Gly Gln Ala Gln Ile
260 265 270

Glu Gly Val Asp Gly Thr Trp Lys Glu Leu Thr Asp Asn Val Asn Val
275 280 285

Met Ala Gln Asn Leu Thr Asp Gln Val Arg Glu Ile Ala Ser Val Thr
290 295 300

Thr Ala Val Ala His Gly Asp Leu Thr Gln Lys Ile Glu Ser Ala Ala
305 310 315 320

Lys Gly Glu Ile Leu Gln Leu Gln Gln Thr Ile Asn Thr Met Val Asp
325 330 335

Gln Leu Arg Thr Phe Ala Ser Glu Val Thr Arg Val Ala Arg Asp Val
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Gly Thr Glu Gly Met Leu Gly Gly Gln Ala Asp Val Glu Gly Val Lys
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Gly Met Trp Asn Glu Leu Thr Val Asn Val Asn Ala Met Ala Asn Asn
370 375 380

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Lys Gly Asp Leu Thr Gln Lys Val Gln Ala Glu Cys Arg Gly Glu Ile
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Phe Glu Leu Lys Asn Thr Ile Asn Ser Met Val Asp Gln Leu Gln Gln
420 425 430

Phe Ala Arg Glu Val Thr Lys Ile Ala Arg Glu Val Gly Thr Glu Gly
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Arg Leu Gly Gly Gln Ala Thr Val His Asp Val Gln Gly Thr Trp Arg
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Asp Leu Thr Glu Asn Val Asn Gly Met Ala Met Asn Leu Thr Thr Gln
465 470 475 480

Val Arg Glu Ile Ala Asn Val Thr Ser Ala Val Ala Ala Gly Asp Leu
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Ser Lys Lys Ile Arg Val Glu Val Lys Gly Glu Ile Leu Asp Leu Lys
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Asn Thr Ile Asn Thr Met Val Asp Arg Leu Gly Thr Phe Ala Phe Glu
515 520 525

Val Ser Lys Val Ala Arg Ala Val Gly Thr Asp Gly Thr Leu Gly Gly
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Gln Ala Gln Val Glu Asn Val Glu Gly Lys Trp Lys Asp Leu Thr Glu
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Asn Val Asn Thr Met Ala Ser Asn Leu Thr Ser Gln Val Arg Gly Ile
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Ser Thr Val Thr Gln Ala Ile Ala Asn Gly Asp Met Ser Arg Lys Ile
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Asp Val Glu Ala Lys Gly Glu Ile Leu Ile Leu Lys Glu Thr Ile Asn
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Asn Met Val Asp Arg Leu Ser Ile Phe Cys Asn Glu Val Gln Arg Val
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Ala Lys Asp Val Gly Val Asp Gly Ile Met Gly Gly Gln Ala Asp Val
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Ala Gly Leu Lys Gly Arg Trp Lys Glu Ile Thr Thr Asp Val Asn Thr
645 650 655

Met Ala Asn Asn Leu Thr Ala Gln Val Arg Ala Phe Gly Asp Ile Thr
660 665 670

Asn Ala Ala Thr Asp Gly Asp Phe Thr Lys Leu Val Glu Val Glu Ala
675 680 685

Ser Gly Glu Met Asp Glu Leu Lys Arg Lys Ile Asn Gln Met Val Tyr

690

695

700

Asn Leu Arg Asp Ser Ile Gln Arg Asn Thr Gln Ala Arg Glu Ala Ala

705

710

715

720

Glu Leu Ala Asn Lys Thr Lys Ser Glu Phe Leu Ala Asn Met Ser His

725

730

735

Glu Ile Arg Thr Pro Met Asn Gly Ile Ile Gly Met Thr Gln Leu Thr

740

745

750

Leu Asp Thr Asp Leu Thr Gln Tyr Gln Arg Glu Met Leu Asn Ile Val

755

760

765

Asn Asn Leu Ala Met Ser Leu Leu Thr Ile Ile Asp Asp Ile Leu Asp

770

775

780

Leu Ser Lys Ile Glu Ala Lys Arg Met Val Ile Glu Glu Ile Pro Tyr

785

790

795

800

Thr Leu Arg Gly Thr Val Phe Asn Ala Leu Lys Thr Leu Ala Val Lys

805

810

815

Ala Asn Asp Lys Phe Leu Asp Leu Thr Tyr Arg Val Asp Ser Ser Val

820

825

830

Pro Asp His Val Ile Gly Asp Ser Phe Arg Leu Arg Gln Ile Ile Leu

835

840

845

Asn Leu Val Gly Asn Ala Ile Lys Phe Thr Glu His Gly Glu Val Ser

850

855

860

Leu Thr Ile Gln Lys Gly Asn Asp Val Thr Cys Leu Pro Asn Glu Tyr

865

870

875

880

Met Ile Glu Phe Val Val Ser Asp Thr Gly Ile Gly Ile Pro Thr Asp

885

890

895

Lys Leu Gly Leu Ile Phe Asp Thr Phe Gln Gln Ala Asp Gly Ser Met

900

905

910

Thr Arg Lys Phe Gly Gly Thr Gly Leu Gly Leu Ser Ile Ser Lys Arg

915

920

925

Leu Val Asn Leu Met Gly Gly Asp Val Trp Val Lys Ser Gln Tyr Gly

930

935

940

Lys Gly Ser Ser Phe Tyr Phe Thr Cys Arg Val Arg Leu Ala Asp Val

945

950

955

960

Asp Ile Ser Leu Ile Arg Lys Gln Leu Lys Pro Tyr Lys Gly His Gln

965

970

975

Val Leu Phe Ile Asp Lys Gly Lys Thr Gly His Gly Pro Glu Val Gly

980

985

990

Gln Met Leu Gly Gln Leu Gly Leu Val Pro Ile Val Leu Glu Ser Glu

995

1000

1005

Gln Asn His Thr Leu Thr Arg Val Arg Gly Lys Glu Cys Pro Tyr
1010 1015 1020

Asp Val Ile Val Val Asp Ser Ile Asp Thr Ala Arg Arg Leu Arg
1025 1030 1035

Gly Ile Asp Asp Phe Lys Tyr Leu Pro Ile Val Leu Leu Ala Pro
1040 1045 1050

Thr Val His Val Ser Leu Lys Ser Cys Leu Asp Leu Gly Ile Thr
1055 1060 1065

Ser Tyr Met Thr Met Pro Cys Lys Leu Ile Asp Leu Gly Asn Gly
1070 1075 1080

Met Val Pro Ala Leu Glu Asn Arg Ala Thr Pro Ser Leu Ser Asp
1085 1090 1095

Asn Thr Lys Ser Phe Glu Ile Leu Leu Ala Glu Asp Asn Thr Val
1100 1105 1110

Asn Gln Arg Leu Ala Val Lys Ile Leu Glu Lys Tyr Asn His Val
1115 1120 1125

Val Thr Val Val Ser Asn Gly Ala Glu Ala Leu Glu Ala Val Lys
1130 1135 1140

Asp Asn Lys Tyr Asp Val Ile Leu Met Asp Val Gln Met Pro Val
1145 1150 1155

Met Gly Gly Phe Glu Ala Thr Ala Lys Ile Arg Glu Tyr Glu Arg
1160 1165 1170

Ser Leu Gly Thr Gln Arg Thr Pro Ile Ile Ala Leu Thr Ala His
1175 1180 1185

Ala Met Met Gly Asp Arg Glu Lys Cys Ile Glu Ala Gln Met Asp
1190 1195 1200

Glu Tyr Leu Ser Lys Pro Leu Gln Gln Asn His Leu Ile Gln Thr
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Ile Leu Lys Cys Ala Thr Leu Gly Gly Ala Leu Leu Glu Gln Asn
1220 1225 1230

Arg Glu Arg Glu Leu Glu Leu Ala Arg His Ala Glu His Lys Gly
1235 1240 1245

Gly Leu Ser Thr Asp Pro Ala Arg Ala Ser Ser Val Met Arg Pro
1250 1255 1260

Pro Leu His His Arg Pro Val Thr Thr Ala Glu Ser Leu Ser Gly
1265 1270 1275

Gly Ala Glu Ser Pro Ser Leu Met Ala Asn Asp Gly Glu Asp Pro
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1295 1300 1305

<210> 17

<211> 1298

<212> PRT

<213> Neurospora crassa

<400> 17

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Thr His Val Arg Leu Pro Gly Pro Tyr Thr Arg Glu Lys Gly Asp Leu
35 40 45

Glu Arg Glu Leu Ser Ala Leu Val Val Arg Ile Glu Gln Leu Glu Thr
50 55 60

Ala Ala Ile Ala Ala Ser Pro Pro Ala Met Pro Asp Thr Pro Asn Ala
65 70 75 80

Pro Thr Asp Ala Leu Phe Ser Asn Gly Thr Leu Ser Pro Ser Ser Glu
85 90 95

Thr Pro Asp Ala Arg Tyr Pro Ala Pro Leu Pro Arg Asn Gly Phe Ile
100 105 110

Asp Glu Ala Leu Glu Gly Leu Arg Glu His Val Asp Asp Gln Ser Lys
115 120 125

Leu Leu Asp Ser Gln Arg Gln Glu Leu Ala Gly Val Asn Ala Gln Leu
130 135 140

Ile Glu Gln Lys Gln Leu Gln Glu Lys Ala Leu Ala Ile Ile Glu Gln
145 150 155 160

Glu Arg Val Ala Thr Leu Glu Arg Glu Leu Trp Lys His Gln Lys Ala
165 170 175

Asn Glu Ala Phe Gln Lys Ala Leu Arg Glu Ile Gly Glu Ile Val Thr
180 185 190

Ala Val Ala Arg Gly Asp Leu Ser Lys Lys Val Arg Met Asn Ser Val
195 200 205

Glu Met Asp Pro Glu Ile Thr Thr Phe Lys Arg Thr Ile Asn Thr Met
210 215 220

Met Asp Gln Leu Gln Val Phe Ser Ser Glu Val Ser Arg Val Ala Arg
225 230 235 240

Glu Val Gly Thr Glu Gly Ile Leu Gly Gly Gln Ala Gln Ile Glu Gly
245 250 255

Val Asp Gly Thr Trp Lys Glu Leu Thr Asp Asn Val Asn Val Met Ala
260 265 270

Gln Asn Leu Thr Asp Gln Val Arg Glu Ile Ala Ser Val Thr Thr Ala
275 280 285

Val Ala His Gly Asp Leu Thr Lys Lys Ile Glu Arg Pro Ala Lys Gly
290 295 300

Glu Ile Leu Gln Leu Gln Gln Thr Ile Asn Thr Met Val Asp Gln Leu
305 310 315 320

Arg Thr Phe Ala Ser Glu Val Thr Arg Val Ala Arg Asp Val Gly Thr
325 330 335

Glu Gly Ile Leu Gly Gly Gln Ala Asp Val Glu Gly Val Gln Gly Met
340 345 350

Trp Asn Glu Leu Thr Val Asn Val Asn Ala Met Ala Asn Asn Leu Thr
355 360 365

Thr Gln Val Arg Asp Ile Ile Lys Val Thr Thr Ala Val Ala Lys Gly
370 375 380

Asp Leu Thr Gln Lys Val Gln Ala Glu Cys Arg Gly Glu Ile Phe Glu
385 390 395 400

Leu Lys Lys Thr Ile Asn Ser Met Val Asp Gln Leu Gln Gln Phe Ala
405 410 415

Arg Glu Val Thr Lys Ile Ala Arg Glu Val Gly Thr Glu Gly Arg Leu
420 425 430

Gly Gly Gln Ala Thr Val His Asp Val Gln Gly Thr Trp Arg Asp Leu
435 440 445

Thr Glu Asn Val Asn Gly Met Ala Met Asn Leu Thr Thr Gln Val Arg
450 455 460

Glu Ile Ala Lys Val Thr Thr Ala Val Ala Lys Gly Asp Leu Thr Lys
465 470 475 480

Lys Ile Gly Val Glu Val Gln Gly Glu Ile Leu Asp Leu Lys Asn Thr
485 490 495

Ile Asn Thr Met Val Asp Arg Leu Gly Thr Phe Ala Phe Glu Val Ser
500 505 510

Lys Val Ala Arg Glu Val Gly Thr Asp Gly Thr Leu Gly Gly Gln Ala
515 520 525

Gln Val Asp Asn Val Glu Gly Lys Trp Lys Asp Leu Thr Glu Asn Val
530 535 540

Asn Thr Met Ala Ser Asn Leu Thr Ser Gln Val Arg Gly Ile Ser Thr
545 550 555 560

Val Thr Gln Ala Ile Ala Asn Gly Asp Met Ser Arg Lys Ile Glu Val
565 570 575

Glu Ala Lys Gly Glu Ile Leu Ile Leu Lys Glu Thr Ile Asn Asn Met
580 585 590

Val Asp Arg Leu Ser Ile Phe Cys Asn Glu Val Gln Arg Val Ala Lys
595 600 605

Asp Val Gly Val Asp Gly Ile Met Gly Gly Gln Ala Asp Val Ala Gly
610 615 620

Leu Lys Gly Arg Trp Lys Glu Ile Thr Thr Asp Val Asn Thr Met Ala
625 630 635 640

Asn Asn Leu Thr Ala Gln Val Arg Ala Phe Gly Asp Ile Thr Asn Ala
645 650 655

Ala Thr Asp Gly Asp Phe Thr Lys Leu Val Glu Val Glu Ala Ser Gly
660 665 670

Glu Met Asp Glu Leu Lys Lys Lys Ile Asn Gln Met Val Tyr Asn Leu
675 680 685

Arg Asp Ser Ile Gln Arg Asn Thr Gln Ala Arg Glu Ala Ala Glu Leu
690 695 700

Ala Asn Lys Thr Lys Ser Glu Phe Leu Ala Asn Met Ser His Glu Ile
705 710 715 720

Arg Thr Pro Met Asn Gly Ile Ile Gly Met Thr Gln Leu Thr Leu Asp
725 730 735

Thr Asp Leu Thr Gln Tyr Gln Arg Glu Met Leu Asn Ile Val Asn Ser
740 745 750

Leu Ala Asn Ser Leu Leu Thr Ile Ile Asp Asp Ile Leu Asp Leu Ser
755 760 765

Lys Ile Glu Ala Arg Arg Met Val Ile Glu Glu Ile Pro Tyr Thr Leu
770 775 780

Arg Gly Thr Val Phe Asn Ala Leu Lys Thr Leu Ala Val Lys Glu Thr
785 790 795 800

Glu Lys Phe Leu Asp Leu Thr Tyr Arg Val Asp His Ser Val Pro Asp
805 810 815

His Val Val Gly Asp Ser Phe Arg Leu Arg Gln Ile Ile Leu Asn Leu
820 825 830

Val Gly Asn Ala Ile Lys Phe Thr Glu His Gly Glu Val Ser Leu Thr
835 840 845

Ile Gln Lys Ala Ser Ser Val Gln Cys Ser Thr Glu Glu Tyr Ala Ile
850 855 860

Glu Phe Val Val Ser Asp Thr Gly Ile Gly Ile Pro Ala Asp Lys Leu
865 870 875 880

Asp Leu Ile Phe Asp Thr Phe Gln Gln Ala Asp Gly Ser Met Thr Arg
885 890 895

Lys Phe Gly Gly Thr Gly Leu Gly Leu Ser Ile Ser Lys Arg Leu Val
900 905 910

Asn Leu Met Gly Gly Asp Val Trp Val Lys Ser Glu Tyr Gly Lys Gly
915 920 925

Ser Lys Phe Phe Thr Cys Val Val Arg Leu Ala Asn Asp Asp Ile
930 935 940

Ser Leu Ile Ala Lys Gln Leu Asn Pro Tyr Lys Ser His Gln Val Leu
945 950 955 960

Phe Ile Asp Lys Gly Arg Thr Gly His Gly Pro Glu Ile Ala Lys Met
965 970 975

Leu His Gly Leu Gly Leu Val Pro Ile Val Val Asp Ser Glu Arg Asn
980 985 990

Pro Ala Leu Glu Lys Ala Arg Ala Ala Gly Gln Ala Pro Tyr Asp Val
995 1000 1005

Ile Ile Val Asp Ser Ile Glu Asp Ala Arg Arg Leu Arg Ser Val Asp
1010 1015 1020

Asp Phe Lys Tyr Leu Pro Ile Val Leu Leu Ala Pro Val Val His Val
1025 1030 1035 1040

Ser Leu Lys Ser Cys Leu Asp Leu Gly Ile Thr Ser Tyr Met Thr Thr
1045 1050 1055

Pro Cys Gln Leu Ile Asp Leu Gly Asn Gly Met Val Pro Ala Leu Glu
1060 1065 1070

Asn Arg Ala Thr Pro Ser Leu Ala Asp Asn Thr Lys Ser Phe Glu Ile
1075 1080 1085

Leu Leu Ala Glu Asp Asn Thr Val Asn Gln Arg Leu Ala Val Lys Ile
1090 1095 1100

Leu Glu Lys Tyr His His Val Val Thr Val Val Gly Asn Gly Glu Glu
1105 1110 1115 1120

Ala Val Glu Ala Val Lys Arg Lys Lys Phe Asp Val Ile Leu Met Asp
1125 1130 1135

Val Gln Met Pro Ile Met Gly Gly Phe Glu Ala Thr Ala Lys Ile Arg
1140 1145 1150

Glu Tyr Glu Arg Ser Leu Gly Ser Gln Arg Thr Pro Ile Ile Ala Leu
1155 1160 1165

Thr Ala His Ala Met Met Gly Asp Arg Glu Lys Cys Ile Gln Ala Gln
1170 1175 1180

Met Asp Glu Tyr Leu Ser Lys Pro Leu Gln Gln Asn His Leu Ile Gln
1185 1190 1195 1200

Thr Ile Leu Lys Cys Ala Thr Leu Gly Gly Gln Leu Leu Glu Lys Asn
1205 1210 1215

Arg Glu Arg Glu Leu Thr Arg Ala Ala Asp Ala Val Thr Gly Gly Arg
1220 1225 1230

Arg Asp Asn Gly Met Tyr Ser Ala Ser Gln Ala Ala Gln His Ala Ala
1235 1240 1245

Leu Arg Pro Pro Leu Ala Thr Arg Gly Leu Thr Ala Ala Asp Ser Leu
1250' 1255 1260

Val Ser Gly Leu Glu Ser Pro Ser Ile Val Thr Ala Asp Lys Glu Asp
1265 1270 1275 1280

Pro Leu Ser Arg Ala Arg Ala Ser Leu Ser Glu Pro Asn Ile His Lys
1285 1290 1295

Ala Ser